## WHAT IS CLAIMED IS:

l	1. A method of controlling cancer suppression in a mammal having a
2	cancer suppressing gene, comprising the steps of:
3	making a substantially duplicated genetic material corresponding to the
1	genetic material of said gene, the substantially duplicated material selected from the group
5	consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing
5	gene, homologues thereof, fragments thereof, and mixtures thereof; and
7	interchanging said duplicated genetic material and the cancer suppressing gene
3	of the mammal.
l	2. A method of claim 1, wherein before said making a substantially
2	duplicated genetic material, determining the chromosomal location of said cancer suppressing
3	gene of the mammal.
ļ	3. A method of claim 1, wherein after said making a substantially
2	duplicated genetic material, detecting the presence or absence of an inactive cancer
3	suppressing gene of a tissue sample of the mammal to determine whether or not the tissue
1	sample cancer suppressing gene is defective or absent.
l	4. A method of claim 3, wherein in response to a determination that the
2	tissue sample cancer suppressing gene is either defective or absent, replacing a cancer
3	suppressing gene of the mammal with its clone.
l	5. A method of claim 3, wherein the determination of whether or not the
2	tissue sample cancer suppressing gene is defective or absent is accomplished by measuring
3	the amount of protein product of said cancer suppressing gene, of the tissue sample, bound by
1	an antibody specific for said protein.
Į	6. A method of claim 5, wherein the determination of whether or not the
2	tissue sample cancer suppressing gene is defective or absent is accomplished by:
3	(a) labeling said tissue sample with radioactive isotope;
1	(b) lysing the labeled tissue;
5	(c) reacting the protein product of said cancer suppressing gene with an
5	antibody specific for said protein thereby forming a protein/antibody immunocomplex;
7	(d) autoradiographing the immunocomplex obtained in step (c); and

8	(e) determining the presence or absence of the protein product by
9	comparing the autoradiogram of step (d) with the autoradiogram of the standard protein
10	product.
1	7. The method of claim 5, wherein the determination of whether or not
1	
2	the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme
3	immunoassay techniques.
1	8. The method of claim 5, wherein the determination of whether or not
2	the tissue sample cancer suppressing gene is defective or absent is accomplished by
3	immunocytochemistry methods.
1	9. The method of claim 5, wherein the cancer suppressing gene is the RB
2	gene and the protein product is ppRB <sup>110</sup> .
1	10. The method of claim 1, wherein said cancer suppressing gene is
2	replaced with substantially duplicated material selected from the group consisting of said
3	cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures
4	thereof, for therapeutic purposes.
1	11. The method of claim 1, wherein said cancer suppressing gene is
2	replaced with substantially duplicated material selected from the group consisting of said
3	defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures
4	thereof, for facilitating the testing of the carcinogenicity of environmental influences.
1	12. The method of claim 2, wherein the location of said cancer suppressing
2	gene is determined by chromosome walking.
2	gene is determined by enformosome warking.
1	13. The method of claim 2, wherein the location of said cancer suppressing
2	gene is determined through organic markers.
1 .	14. A method of claim 2, wherein:
2	said chromosomal location of said cancer suppressing gene is determined by
3	testing genes of a chromosome for phenotypic expression;
4	determining one of the genes of said chromosome to be a marker gene; and
5	using chromosomal walking techniques to locate a cancer suppressing gene.

1	15. An animal genetically altered so as to have the allele of at least one
2	cancer suppressing gene selected from the group consisting of a defective allele, a homologue
3	thereof, a fragment thereof, and a mixture thereof.
1	16. An animal of claim 15, wherein said defective allele is selected from
2	the group consisting of defective alleles of RB genes, breast cancer suppressing genes,
3	Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes,
4	bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes,
5	small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes,
6	acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homolgues
7	thereof, fragments thereof, and mixtures thereof.
1	17. An animal of claim 15, wherein said allele contains a DNA fragment
2	having at least one defective nucleotide sequence.
1	18. An animal of claim 15, wherein said defective allele contains a DNA
2	fragment having at least one defective RB nucleotide sequence.
1	19. The animal of claim 15, wherein said animal is a mouse.
1	20. A method for determining the carcinogenicity of suspected
2	environmental influences, using the animal of claim 14, comprising the steps of:
3	exposing said animal to a suspected environmental influence;
4	observing the animal for the phenotypic expression of cancer; and
5	determining carcinogenicity of the suspected environmental influence in
6	response to observing a phenotypic expression of cancer in the animal.
1	21. A method of claim 20, wherein said exposing includes exposing to a
2	source of radiation.
1	22. A method of claim 20, wherein said exposing includes exposing to
2	tobacco combustion products.
1	23. A method of claim 20, wherein said exposing includes exposing to
2	food additives.

1	24. A method of claim 20, wherein said exposing includes exposing to
2	artificial substances.
1	25. A method of claim 20, wherein said observing includes examining the
2	animal for tumor development.
1	26. A method of claim 25, wherein in response to the formation of a tumor
2	in the animal, analyzing the tumor for the presence of cancer cells.
1	27. A method of making the animal of claim 15, comprising:
2	using at least one allele of an animal cancer suppressing gene selected from
3	the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a
4	mixture thereof;
5	mutating at least one animal cell with said allele to form a mutated cell;
6	introducing said mutated cell into an animal blastocyst;
7	permitting growth of the blastocyst for a given period of time sufficient to
8	incorporate said allele into its cells; repressing genetic recombinations within said cells;
9	transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal
0	for giving birth subsequently to an animal bearing said allele;
1	breeding said animal to reproduce additional animals; and
12	selecting the animal of claim 14 from said additional animals by determining
13	the presence therein of the said allele.
1	28. A method of claim 27, wherein before introducing said allele,
2	removing said blastocyst from a super ovulated animal, and wherein said blastocyst is
3	comprised of undifferentiated cells.
1	29. A method of claim 27, wherein said introducing is performed in vitro.
1	30. A pharmaceutical composition wherein the active ingredient is selected
2	from the group consisting of a naturally occurring intact cancer suppressing gene, a cloned
3	intact cancer suppressing gene, fragments thereof, homolgues thereof and mixtures thereof.
1	31. A pharmaceutical composition of claim 30, wherein said naturally
2	occurring and cloned cancer suppressing gene is selected from the group consisting of RB
3	genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-

- 4 Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing
- 5 genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal
- 6 cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma
- 7 suppressing genes, homolgues thereof, fragments thereof, and mixtures thereof.
- 1 32. A pharmaceutical composition of claim 30, wherein the active
- 2 ingredient is selected from the group consisting of RB cDNA, modified RB cDNA fragment,
- 3 clones thereof, homolgues thereof and mixtures thereof.

3

- 1 33. A pharmaceutical composition of claim 31, wherein the active
- 2 ingredient for each of said gene is selected from the group consisting od cDNA of said gene,
- 3 fragments of said cDNA, homologues thereof and mixtures thereof.
- 1 34. A pharmaceutical composition of claim 32, wherein the cancer
- 2 suppressing gene is isolated from human chromosome 13 region 13q14.
- 1 35. A pharmaceutical composition of claim 31, wherein the cancer
- 2 suppressing gene and its clone each has the following nucleotide sequence:

5	TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG GGCGTGCCCC GCGTGCGCC GCGTCGTCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC															3	60
6 7	GGCGTGC	CCC ·	GCGT	GCGCC	GC GC	CGTCG	TCCI	ccc	CGGC	CGCT	CCTC	CACA	GC I	CGCT	GGCT	C	120
8 9 10 11	CCGCCGC	GGA	AAGGO	CGTC	ATG Met 1	CCG Pro	CCC Pro	AAA Lys	ACC Thr 5	CCC Pro	CGA Arg	AAA Lys	ACG Thr	GCC Ala 10	GCC Ala		171
12 13 14 15	ACC GCC Thr Ala	GCC Ala	GCT Ala 15	GCC Ala	GCC Ala	GCG Ala	GAA Glu	CCC Pro 20	CCG Pro	GCA Ala	CCG Pro	CCG Pro	CCG Pro 25	CCG Pro	CCC Pro		219
16 17 18 19	CCT CCC	TAG Glu 30	Glu	GAC Asp	CCA Pro	GAG Glu	CAG Gln 35	GAC Asp	AGC Ser	GGC Gly	CCG Pro	GAG Glu 40	GAC Asp	CTG Leu	CCT Pro		267
20 21 22 23	CTC GTC Leu Val	Arg	CTT Leu	GAG Glu	TTT Phe	GAA Glu 50	GAA Glu	ACA Thr	GAA Glu	GAA Glu	CCT Pro 55	GAT Asp	TTT Phe	ACT Thr	GCA Ala		315
24 25 26 27	TTA TGT Leu Cys 60	CAC Glr	AAA Lys	TȚA Leu	AAG Lys 65	ATA Ile	CCA Pro	GAT Asp	CAT His	GTC Val 70	Arg	GAG Glu	AGA Arg	GCT Ala	TGG Trp 75		363
28 29 30 31	TTA AC' Leu Th	r TGC r Trp	GAG Glu	AAA Lys 80	Val	TCA Ser	TCT Ser	GTG Val	GAT Asp 85	Gly	GTA Val	TTG Leu	GGA Gly	GGT Gly 90	TAT Tyr		411

33 34 35	ATT	CAA Gln	AAG Lys	AAA Lys 95	AAG Lys	GAA Glu	CTG Leu	TGG Trp	GGA Gly 100	ATC Ile	TGT Cys	ATC Ile	TTT Phe	ATT Ile 105	GCA Ala	GCA Ala		459
36 37 38 39	GTT Val	GAC Asp	CTA Leu 110	GAT Asp	GAG Glu	ATG Met	TCG Ser	TTC Phe 115	ACT Thr	TTT Phe	ACT Thr	GAG Glu	CTA Leu 120	CAG Gln	AAA Lys	AAC Asn		507
40 41 42 43	ATA Ile	GAA Glu 125	ATC Ile	AGT Ser	GTC Val	CAT His	AAA Lys 130	TTC Phe	TTT Phe	AAC Asn	TTA Leu	CTA Leu 135	AAA Lys	GAA Glu	ATT Ile	GAT Asp		555
44 45 46 47	ACC Thr 140	AGT Ser	ACC Thr	AAA Lys	GTT Val	GAT Asp 145	AAT Asn	GCT Ala	ATG Met	TCA Ser	AGA Arg 150	CTG Leu	TTG Leu	AAG Lys	AAG Lys	ТАТ Туг 155		603
48 49 50 51	GAT Asp	GTA Val	TTG. Leu	TTT Phe	GCA Ala 160	CTC Leu	TTC Phe	AGC Ser	AAA Lys	TTG Leu 165	GAA Glu	AGG Arg	ACA Thr	TGT Cys	GAA Glu 170	CTT Leu		651
52 53 54 55	ATA Ile	TAT Tyr	TTG Leu	ACA Thr 175	CAA Gln	CCC Pro	AGC Ser	AGT Ser	TCG Ser 180	ATA Ile	TCT Ser	ACT Thr	GAA Glu	ATA Ile 185	AAT Asn	TCT Ser	٠	699
56 57 58 59	GCA Ala	TTG Leu	GTG Val 190	CTA Leu	AAA Lys	GTT Val	TCT Ser	TGG Trp 195	ATC Ile	ACA Thr	TTT	TTA Leu	TTA Leu 200	GCT Ala	AAA Lys	GGG Gly		747
60 61 62 63	Glu	Val 205	Leu	Gln	Met	Glu	Asp 210	Asp	Leu	Val	Ile	Ser 215	Phe	CAG Gln	Leu	Met		795 843
64 65 66 67	Leu 220	Cys	Val	Leu	Asp	Tyr 225	Phe	Ile	Lys	Leu	Ser 230	Pro	Pro		Leu	Leu 235		
68 69 70 71	AAA Lys	GAA Glu	CCA Pro	TAT Tyr	AAA Lys 240	ACA Thr	GCT Ala	GTT Val	ATA Ile	CCC Pro 245	ATT Ile	AAT Asn	GGT Gly	TCA Ser	Pro 250	CGA Arg		891
72 73 74 75	ACA Thr	CCC Pro	AGG Arg	CGA Arg 255	Gly	CAG Gln	AAC Asn	AGG Arg	AGT Ser 260	Ala	CGG Arg	ATA Ile	GCA Ala	AAA Lys 265	Gln	CTA Leu		939
76 77 78 79	GAA Glu	AAT Asn	GAT Asp 270	Thr	AGA Arg	ATT	ATT Ile	GAA Glu 275	Val	CTC Leu	TGT Cys	AAA Lys	GAA Glu 280	His	GAA Glu	TGT Cys		987
80 81 82	AAT Asn	ATA Ile 285	Asp	GAG Glu	GTG Val	AAA Lys	AAT Asn 290	Val	TAT	TTC Phe	Lys	AAT Asn 295	Phe	ATA : Ile	CCT Pro	TTT Phe		1035
83 84 85 86	ATG Met 300	Asn	TCT Ser	CTT Leu	GGA Gly	CTT Leu 305	GTA Val	ACA Thr	TCT Ser	AAT Asn	GGA Gly 310	Leu	CCA Pro	GAG Glu	GTT Val	GAA Glu 315		1083
87 88 89 90	AAT Asn	CTI Leu	TCT Ser	AAA Lys	CGA Arg 320	Tyr	GAA Glu	GAA Glu	ATT i Ile	TAT Tyr 325	Leu	AAA Lys	AA7 Asr	AAA Lys	GAT Asp 330	CTA Leu		1131
91 92 93	GAT Asp	GCA Ala	A AGA Arg	TTA Lev	TTI i Phe	TTG Leu	GAT Asp	CAT His	GAT S Asp	AAA Lys	ACT Thr	CTI Lev	CAC Glr	ACT Thi	GAT Asp	TCT Ser		1179

94 95				335					340					345			•
96 97 98						ACA Thr											1227
99 100 101			GTG			ATT Ile		CCA									1275
102 103 104	AAC	365 ACT	ATC	CAA	CAA	TTA	370 ATG	ATG	ATT	TTA	TÂA	375 TCA	GCA	AGT	GAT	CAA	1323
105 106 107	380					Leu 385	-				390					395	1071
108 109 110						ATT Ile											1371
111 112 113 114						AAA Lys											1419
115 116 117 118						GCT Ala											1467
119 120 121 122						GGA Gly											1515
123 124 125 126	ATO Met 460	G CT' Leu	r AA/ Lys	A TC Ser	A GAZ Glu	A GAZ Glu 465	A GAA	A CG <i>l</i> Arg	A TT <i>l</i> Leu	A TCC Ser	Ile 470	Г САЛ Gln	A AA' Asn	r TT Phe	r AG0 Ser	C AAA Lys 475	1563
127 128 129 130	CTT Leu	CTG Leu	AAT Asn	GAC Asp	AAC Asn 480	ATT Ile	TTT Phe	CAT His	ATG Met	TCT Ser 485	TTA Leu	TTG Leu	GCG Ala	TGC Cys	GCT Ala 490	CTT Leu	1611
131 132 133 134 135						ACA Thr											1659
136 137 138 139	TCT Ser	GGA Gly	ACA Thr 510	GAT Asp	TTG Leu	TCT Ser	TTC Phe	CCA Pro 515	TGG Trp	ATT Ile	CTG Leu	AAT Asn	GTG Val 520	CTT	AAT Asn	TTA Leu	1707
140 141 142 143	AAA Lys	GCC Ala	TTT	GAT	TTT	TAC Tvr	AAA Lvs	GTG Val	ATC	GAA Glu	AGT	TTT Phe	ATC	AAA Lvs	GCA Ala	GAA Glu	1755
175	•	525		мар	1110	-1-	530	vai	110	014	BCI	535	110	- <b>1</b> -			
144 145 146 147	GGC	525 AAC Asn	TTG	ACA	AGA	GAA Glu 545	530 ATG	ATA	AAA	CAT	TTA	535 GAA	CGA	TGT	GAA	CAT	1803
145	GGC Gly 540 CGA	525 AAC Asn	TTG Leu ATG	ACA Thr	AGA Arg	GAA Glu 545 CTT Leu	ATG Met	ATA Ile	AAA Lys CTC	CAT His	TTA Leu 550 GAT	GAA Glu TCA	CGA Arg	TGT Cys TTA	GAA Glu TTT	CAT His 555	1803

155 156 157 158	TCT Ser	GCT Ala	TGT Cys 590	CCT Pro	CTT Leu	AAT Asn	CTT Leu	CCT Pro 595	CTC Leu	CAG Gln	AAT Asn	AAT Asn	CAC His 600	ACT Thr	GCA Ala	GCA Ala	1947
159 160 161 162	GAT Asp	ATG Met 605	TAT Tyr	CTT Leu	TCT Ser	CCT Pro	GTA Val 610	AGA Arg	TCT Ser	CCA Pro	AAG Lys	AAA Lys 615	AAA Lys	GGT Gly	TCA Ser	ACT Thr	1995
163 164 165 166	ACG Thr 620	CGT Arg	GTA Val	AAT Asn	TCT Ser	ACT Thr 625	GCA Ala	AAT Asn	GCA Ala	GAG Glu	ACA Thr 630	CAA Gln	GCA Ala	ACC Thr	TCA Ser	GCC Ala 635	2043
167 168 169 170	TTC Phe	CAG Gln	ACC Thr	CAG Gln	AAG Lys 640	CCA Pro	TTG Leu	AAA Lys	TCT Ser	ACC Thr 645	TCT Ser	CTT Leu	TCA Ser	CTG Leu	TTT Phe 650	TAT Tyr	2091
171 172 173 174	AAA Lys	AAA Lys	GTG Val	TAT Tyr 655	CGG Arg	CTA Leu	GCC Ala	TAT Tyr	CTC Leu 660	CGG Arg	CTA Leu	AAT Asn	ACA Thr	CTT Leu 665	TGT Cys	GAA Glu	2139
175 176 177 178	CGC Arg	CTT Leu	CTG Leu 670	TCT Ser	GAG Glu	CAC His	CCA Pro	GAA Glu 675	TTA Leu	GAA Glu	CAT His	ATC Ile	ATC Ile 680	TGG Trp	ACC Thr	CTT Leu	2187
179 180 181 182	TTC Phe	CAG Gln 685	CAC His	ACC Thr	CTG Leu	CAG Gln	AAT Asn 690	GAG Glu	TAT Tyr	GAA Glu	CTC Leu	ATG Met 695	AGA Arg	GAC Asp	AGG Arg	CAT His	2235
183 184 185 186	TT Leu 700	G GA Asp	C. CA	A AT	T AT Met	G ATO Met 705	G TG' Cys	r TC Ser	C ATO	G TA' Tyr	T GG Gly 710	C AT.	A TG Cys	C AA Lys	A GT Val	G AAG Lys 715	2283
187 188 189 190	AAT Asn	ATA Ile	GAC Asp	CTT Leu	AAA Lys 720	Phe	AAA Lys	ATC Ile	ATT Ile	GTA Val 725	ACA Thr	GCA Ala	TAC	AAG Lys	GAT Asp 730	CTT Leu	2331
191 192 193 194	CCT Pro	CAT His	GCT Ala	GTT Val	Gln	GAG Glu	ACA Thr	TTC Phe	AAA Lys 740	Arg	GTT Val	TTG Leu	ATC	AAA Lys 745	Glu	GAG Glu	2379
195 196 197 198	GAG Glu	TAT	GAT Asp 750	Ser	ATT	ATA Ile	Val	Phe	TAT Tyr	Asn	Ser	Val	Phe	Met	CAG Gln	AGA Arg	2427
199 200 201 202	CTG Leu	AAA Lys	Thr	AAT Asn	'ATT	TTG Leu	CAG Gln 770	Tyr	GCT Ala	TCC Ser	ACC Thr	AGG Arg	Pro	CCT Pro	ACC Thr	TTG Leu	2475
203 204 205 206	TCA Ser	Pro	ATA Ile	CCT	CAC His	ATT	Pro	CGA Arg	AGC Ser	CCT	TAC Tyr 790	Lys	TTI Phe	CCT Pro	AGT Ser	TCA Ser 795	2523
207 208 209 210	CCC Pro	TTA Leu	A CGG	ATT	C CCT Pro 800	Gly	GGG Gly	AAC Asr	: ATC	TAT Tyr 805	: Ile	TCA Ser	CCC Pro	C CTC	B AAC 1 Lys 810	G AGT S Ser	2571
211 212 213	CCF	TAT	T AAA	ALATI	r TCF	A GAA	GGI	CTC	CCA	ACA	A CCI	A AC	AAA	ATC	AC	CCA	2619

216 217 218 219	AGA Arg	TCA Ser	AGA Arg 830	ATC Ile	TTA Leu	GTA Val	TCA Ser	ATT Ile 835	GGT Gly	GAA Glu	TCA Ser	TTC Phe	GGG Gly 840	ACT Thr	TCT Ser	GAG Glu	2667
220 221 222 223	AAG Lys	TTC Phe 845	CAG Gln	AAA Lys	ATA Ile	AAT Asn	CAG Gln 850	Met	GTA Val	TGT Cys	AAC Asn	AGC Ser 855	GAC Asp	CGT Arg	GTG Val	CTC Leu	2715
224 225 226 227	AAA Lys 860	AGA Arg	AGT Ser	GCT Ala	GAA Glu	GGA Gly 865	AGC Ser	AAC Asn	CCT Pro	CCT Pro	AAA Lys 870	CCA Pro	CTG Leu	AAA Lys	AAA Lys	CTA Leu 875	2763
228 229 230 231	CGC Arg	TTT Phe	GAT Asp	ATT Ile	GAA Glu 880	GGA Gly	TCA Ser	GAT Asp	GAA Glu	GCA Ala 885	GAT Asp	GGA Gly	AGT Ser	AAA Lys	CAT His 890	CTC Leu	2811
232 233 234	CCA Pro	GGA Gly	GAG Glu	TCC Ser 895	AAA Lys	TTT Phe	CAG Gln	CAG Gln	AAA Lys 900	CTG Leu	GCA Ala	GAA Glu	ATG Met	ACT Thr 905	TCT Ser	ACT Thr	2859
235 236 237 238 239	CGA Arg	ACA Thr	CGA Arg 910	ATG Met	CAA Gln	AAG Lys	CAG Gln	AAA Lys 915	ATG Met	AAT Asn	GAT	AGC Ser	ATG Met 920	GAT Asp	ACC Thr	TCA Ser	2907
240 241 242				GAG Glu			GGAT	CTC .	AGGA	CCTT	GG T	GGAC.	ACTG	T GT.	ACAC	CTCT	2962
243 244	GGA	TTCA	TTG	TCTC	TCAC.	AG A	TGTG	ACTG	T AT								2994

- 1 36. A pharmaceutical composition of claim 32, wherein said RB cDNA
- 2 fragment is selected from the group consisting of RB-1, RB-2, RB-5, y79R8 and mixtures
- 3 thereof.
- 1 37. A pharmaceutical composition of claim 32, wherein a resulting mRNA
- 2 transcript of said RB cDNA fragment has 4.6 kb.
- 1 38. A pharmaceutical composition of claim 37, wherein the cloned
- 2 genomic DNA has at least 27 exons.
- 1 39. A pharmaceutical composition of claim 30, wherein the cloned RB
- 2 cDNA transcribes into mRNA which translates in protein having an amino acid sequence
- 3 comprising:

	·	/ 2.43
4	MPPKTPRKT <u>AATAAAAA</u> E <u>PPAPPPPPPP</u> EEDPE	( 34)
5	ODSGPEDLPLVRLEFEETEEPDFTALCQKLKIPDHVRERA	(74)
6	WLTWEKVSSVDGVLGGYIQKKKELWGICIFIAAVDLDEMS	(114)
7	FTFTELOKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKK	(154)
8	YDVLFALFSKLERTCELIYLTQPSSSISTEINSALVLKVS	(194)
9	WITFLLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML	(234)
10	LKEPYKTAVIPINGSPRTPRRGQMRSARIAKQLENDTRII	(274)
11	EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	(314)
12	ENLSKRYEEIYLKNKDLDARLFLDHDKTLQTDSIDSFETQ	(354)
13	RTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSASD	(394)
14	OPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAV	(434)
15	GOGCVEIGSORYKLGVRLYYRVMESMLKSEEERLSIQNFS	(474)
16	KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSF	(514)
17	PWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCE	(554)
18	HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL	(594)
19	PLONNHTAADMYLSPVRSPKKKGSTTRVNSTANAETQATS	(634)
20	AFOTOKPLKSTSLSLFYKKVYRLAYLRLNŢLCERLLSEHP	(674)
21	ELEHIIWTLFOHTLQNEYELMRDRHLDQIMMCSMYGICKV	(714)
22	KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIV	(754)
23	FYNSVFMORLKTNILQYASTRPPTLSPIPHIPRSPYKFPS	(794)
24	SPLRIPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVS	(834)
25	IGESFGTSEKFQKINQMVCNSDRVLKRSAEGSNPPKPLKK	(874)
26	LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ	(914)
27	KMNDSMDTSNKEEK	(928)
28	, , , , , , , , , , , , , , , , , , ,	
29		

single-letter abbreviations for the amino acid residues are: A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

## A DNA nucleotide sequence comprising: 40.

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG GGCGTGCCCC GCGTGCGCC GCGTCGTCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC 7 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG

24 25 26	Leu 60	Cys	Gln	Lys	Leu	Lys 65	Ile	Pro	Asp	His	Val 70	Arg	Glu	Arg	Ala	Trp 75		
27 28 29	TTA Leu	ACT Thr	TGG Trp	GAG Glu	AAA Lys 80	GTT Val	TCA Ser	TCT Ser	GTG Val	GAT Asp 85	Gly	GTA Val	TTG Leu	GGA Gly	GGT Gly 90	TAT Tyr	4	11
30 31 32 33 34	ATT Ile	CAA Gln	AAG Lys	AAA Lys 95	AAG Lys	GAA Glu	CTG Leu	TGG Trp	GGA Gly 100	ATC Ile	TGT Cys	ATC Ile	TTT Phe	ATT Ile 105	GCA Ala	GCA Ala	4	59
35 36 37 38	GTT Val	GAC Asp	CTA Leu 110	GAT Asp	GAG Glu	ATG Met	TCG Ser	TTC Phe 115	ACT Thr	TTT Phe	ACT Thr	GAG Glu	CTA Leu 120	CAG Gln	AAA Lys	AAC Asn	5	07
39 40 41 42	ATA Ile	GAA Glu 125	ATC Ile	AGT Ser	GTC Val	CAT	AAA Lys 130	TTC Phe	TTT Phe	AAC Asn	TTA Leu	CTA Leu 135	AAA Lys	GAA Glu	ATT	GAT Asp	5	555
43 44 45 46	ACC Thr 140	Ser	ACC Thr	AAA Lys	GTT Val	GAT Asp 145	AAT Asn	GCT Ala	ATG Met	TCA Ser	AGA Arg 150	CTG Leu	TTG Leu	AAG Lys	AAG Lys	TAT Tyr 155	6	503
47 48 49 50	GAT Asp	GTA Val	TTG Leu	TTT Phe	GCA Ala 160	CTC Leu	TTC Phe	AGC Ser	AAA Lys	TTG Leu 165	GAA Glu	AGG Arg	ACA Thr	TGT Cys	GAA Glu 170	CTT Leu	6	551
51 52 53 54	ATA Ile	TAT Tyr	TTG Leu	ACA Thr 175	CAA Gln	CCC Pro	AGC Ser	AGT Ser	TCG Ser 180	ATA Ile	TCT Ser	ACT Thr	GAA Glu	ATA Ile 185	AAT Asn	TCT	6	599
55 56 57 58	GCA Ala	TTG Leu	GTG Val 190	Leu	AAA Lys	GTT Val	TCT Ser	TGG Trp 195	ATC Ile	ACA Thr	TTT Phe	TTA Leu	TTA Leu 200	GCT Ala	AAA Lys	GGG Gly	•	747
59 60	GAA Glu	Val	Leu	CAA Gln	ATG Met	GAA Glu	GAT Asp 210	GAT Asp	CTG Leu	GTG Val	ATT Ile	TCA Ser 215	Phe	CAG Gln	TTA Leu	ATG Met	•	795
61 62 63 64	CTA Leu 220	Cys	GTC	CTT Leu	GAC Asp	TAT Tyr 225	TTT	ATT Ile	AAA Lys	CTC Leu	TCA Ser 230	CCT Pro	CCC	ATG Met	TTG Leu	CTC Leu 235	1	843
65 66 67 68 69	AAA Lys	GAA Glu	CCA Pro	TAT Tyr	Lys 240	Thr	GCT Ala	GTT Val	ATA Ile	CCC Pro 245	o Il∈	TAA '	GGT Gly	TCA Ser	CCT Pro 250	CGA Arg		891
70 71 72	ACA Thr	CCC Pro	AGC Arg	CGA Arg 255	Gly	CAG Gln	AAC Asn	AGG Arg	AGT Ser 260	Ala	A CGG Arg	B ATA	GCA Ala	AAA Lys 265	GIn	CTA Leu		939
73 74 75 76	GA <i>A</i> Glu	A AAT 1 Asi	GAT Asp 270	Thr	AGA Arg	A ATT	ATT	GAA Glu 275	ı Val	CTC Let	TGT 1 Cys	C AAA S Lys	GAA Glu 280	ı Hıs	GAA Glu	TGT Cys	• .	987
77 78 79 80	AAT Ası	T ATA	e Asp	GAC Glu	GTC u Val	B AAA L Lys	AAT Asn 290	Va]	TAT Tyr	TTC Phe	C AAA	A AAT s Asr 295	n Phe	T ATA	A CCT	TTT Phe	1	.035
81 82 83 84	ATO Met	. Ası	T TC	r CTT	r GGA ı Gly	A CTI y Leu 305	ı Val	ACA Thi	A TCT	AA 1	r GGZ n Gly 31	y Lei	r CCA	A GAC	G GTT 1 Val	GAA Glu 315	1	.083

85																	
86	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
87	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	_	Leu	Lys	Asn	Lys	Asp	Leu	
88					320					325					330		
89 90	C17 FF	<i>aa</i> ,	202	mm 2	mmm		a z m	(1) T	CI N CI	70 70 70	z Cm	OPP.	ara.	7 CI	CI N III	mam	1170
91													_		GAT Asp		1179
92	АБР	Ата	AIG	335	FIIC	Бец	нар	1113	340	шуз	1111	neu	OIII	345	чор	DCI	
93				333					310					313			
94	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
95															Leu		
96		•	350					355			_	-	360			_	
97																	
98	GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
99	Glu		Val	Asn	Val	Ile		Pro	His	Thr	Pro		Arg	Thr	Val	Met	
100		365					370					375					
101		T CIM	3 m.a	~~~	~~~	(T)(T) N	3 ma	7 MIC	2 mm	<b></b>	7 7 CT	max.	aar	» am	(1) III	G 3 3	1222
102 103															GAT		1323
103	380	THE	тте	GIII	GIII	385	Met	Met	116	ьеи	390	ser	Ald	ser	Asp	3.95	
105	300					505										3.23	
106	ССТ	TCA	GAA	ААТ	CTG	АТТ	TCC	ТАТ	ттт	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
107															Asn		
108					400			4 -		405		- 1			410		
109																	
110	AAA	GAA	AGT	ATA	CTG	AAA	AGA	$\operatorname{GTG}$	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
111	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
112				415					420					425			
113													4.2.2				
114															GGA		1467
115 116	GIu	гуs		Ата	гàг	Ата	vaı	_	GIN	GIY	Cys	vaı	440	11e	Gly	ser	
117			430					435					440				
118	CAG	CGA	тас	ΔΔΔ	Стт	GGA	GTT	CGC	TTG	ТАТ	TAC	CGA	GTA	ATG	GAA	TCC	1515
119						_	_						_		Glu	_	
120		445	-1-	1		- 1	450	_		-	•	455					
121																	
122																C AAA	1563
123	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser		Gln	Asn	Phe	Ser		
124	460					465					470					475	
125								a				mma		maa	aam	CITION .	1611
126															GCT		1611
127 128	ьeu			_			Pne								Ala	Leu	
129					400					405					490		
130	GAG	GTT	GTA	ATG	GCC	ACA	тат	AGC	AGA	AGT	ACA	тст	CAG	AAT	CTT	GAT	1659
131															Leu		
132	010	V CL 2		495			-1-		500					505		<b>L</b>	
133																	
134	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	ATT	1707
135	Ser	Gly	Thr	Asp	Leu	Ser	Phe	${\tt Pro}$	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
136			510					515					520				
137																~~~	1000
138															GCA		1755
139	ГЛЗ		Phe	Asp	Phe	Tyr		٧al	TTE	Glu	ser		пте	гàг	Ala	GIU	
140 141		525					530					535					
141	GGG	ልእሮ	Thirt	ልሮኦ	אכים	GAA	אַדית	מידים	ΔΔΔ	СРФ	ጥጥል	CAD	CGD	ጥርጥ	GAA	ТАТ	1803
143															Glu		
144	540	4911	лси	TIL	y	545			_, 5	****	550	Ų. Lu	9	<b>υ</b> γ 5	-14	555	
145																•	

146 147 148 149															TTT Phe 570		1851
150 151 152 153															CTT Leu		1899
154 155 156 157															GCA Ala		1947
158 159 160 161															TCA Ser		1995
162 163 164 165															TCA Ser		2043
166 167 168 169															TTT Phe 650		2091
170 171 172 173															TGT Cys		2139
174 175 176 177										_		_	_		ACC Thr	_	2187
178 179 180 181															AGG Arg		2235
182 183 184 185															A GTO Val	G AAG Lys 715	2283
186 187 188 189															GAT Asp 730		2331
190 191 192 193															GAA Glu	_	2379
194 195	070																
196 197															CAG Gln		2427
	Glu CTG	Tyr AAA	Asp 750 ACA	Ser AAT	Ile ATT	Ile TTG	Val CAG	Phe 755 TAT	Tyr GCT	Asn	Ser	Val AGG	Phe 760 CCC	Met	_	Arg TTG	2427
197 198 199 200	Glu CTG Leu TCA	AAA Lys 765 CCA	Asp 750 ACA Thr	Ser AAT Asn	Ile ATT Ile CAC	Ile TTG Leu	CAG Gln 770 CCT	Phe 755 TAT Tyr	Tyr GCT Ala	TCC Ser	Ser ACC Thr	AGG Arg 775	Phe 760 CCC Pro	Met CCT Pro	Gln	TTG Leu TCA	

207 208 209	Pro	Leu	Arg	Ile	Pro 800	Gly	Gly	Asn	Ile	Tyr 805	Ile	Ser	Pro	Leu	Lys 810	Ser	
210	CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619
211	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	
212		•	-	815			-		820				_	825			
213			ĺ			•											
214	AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2667
215	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	
216	_		830					835					840				
217																	
218	AAG	TTC	CAG	AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	2715
219	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	
220		845					850					855					
221																	
222	AAA	AGA	AGT	GCT	GAA	GGA	AGC	AAC	CCT	CCT	AAA	CCA	CTG	AAA	AAA	CTA	2763
223	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	
224 -	860					865					870					875	
225					-												
226	CGC	TTT	GAT	ATT	GAA	GGA	TCA	GAT	GAA	GCA	GAT	GGA	AGT	AAA	CAT	CTC	2811
227	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	
228					880					885					890		
229																	
230															TCT		2859
231	Pro	Gly	Glu		Lys	Phe	Gln	Gln	-	Leu	Ala	Glu	Met		Ser	Thr	
232				895					900					905			
233			_														
234															ACC		2907
235	Arg	Thr	_	Met	Gln	Lys	Gln	-	Met	Asn	Asp	Ser		Asp	Thr	Ser	
236			910					915					920				
237				~~~						<b></b>			aman			<b></b>	0060
238						TGAC	3GAT(	JTC A	AGGAC	CTTC	G TC	3GAC	ACTG'	r Grz	ACAC	FTCT	2962
239	Asn	-	Glu	GIU.	гÀг												
240		925															
241 242	aar	nmar -	nma n	namaa	пака:		nama	amar	יים גד וז								2994
<b>44</b>	GGA'	T'CA'.	LTG '	rCTC'.	CACA	AG AT	LG TGA	ACTG.	LAT								∠ <del>3 3 4</del>

1 41. A method of therapeutically treating inactive, mutative or absent 2 cancer suppressing genes comprising:

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treating said inactive, mutative or absent cancer suppressing genes with at least a portion of intact cancer suppressing genes.

- 42. A method of claim 41, wherein said cancer suppressing genes are each a substance selected from the groups consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures thereof.
  - 43. A method of claim 41, wherein said treating includes:

2	treating said inactive, mutative or absent cancer suppressing gene with a
3	substance selected from the group consisting of an RB gene, a portion of said gene, or a
4	mixture thereof.
1	44. A method of claim 43, wherein said portion is selected from the group
2	consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.
1	45. The method of claim 41, wherein the intact cancer suppressing gene, or
2	portion thereof, is delivered to the site of a tumor by means of a retrovirus.
1	46. A method of claim 41, wherein the intact cancer suppressing gene, or a
2	portion thereof, is delivered to the site of a tumor by a liposome.
1 ,	47. A method of claim 41, wherein the location of said cancer suppressing
2	gene is determined by utilizing a genetic marker.